

results of **BLAST**

INFO: Blast: Selenocysteine (U) at position 18 replaced by X

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BLASTP 2.2.6 [Apr-09-2003]

SEQ ID NO: 6

**Reference:**

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1051732211-015145-31043

**Query=**

(18 letters)

**Database:** Non-redundant SwissProt sequences

124,969 sequences; 45,635,229 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

No significant similarity found. For reasons why, [click here](#).

Database: Non-redundant SwissProt sequences

Posted date: Apr 27, 2003 11:15 PM

Number of letters in database: 45,635,229

Number of sequences in database: 124,969

Lambda	K	H
0.315	0.126	0.394

**Gapped**

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 1,249,588

Number of Sequences: 124969

Number of extensions: 8041

Number of successful extensions: 6

Number of sequences better than 10.0: 0

Number of HSP's better than 10.0 without gapping: 0

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 6

Number of HSP's gapped (non-prelim): 0

length of query: 18

length of database: 45,635,229

effective HSP length: 0

effective length of query: 24

effective length of database: 45,635,229

effective search space: 1095245496

effective search space used: 1095245496

T: 11

A: 40

X1: 16 ( 7.3 bits)

X2: 38 (14.6 bits)

X3: 64 (24.7 bits)

S1: 41 (21.6 bits)

S2: 58 (26.9 bits)

results of **BLAST**

INFO: Blast: Selenocysteine (U) at position 15 replaced by X

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**BLASTP 2.2.6 [Apr-09-2003]**Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1051732390-018728-3439

**Query=**

(15 letters)

**Database:** Protein sequences derived from the Patent division of GenBank

119,193 sequences; 19,553,006 total letters

If you have any problems or questions with the results of this search please refer to the **BLAST FAQs**

**No significant similarity found.** For reasons why, [click here](#).

Database: Protein sequences derived from the Patent division of GenBank

Posted date: Apr 27, 2003 10:43 PM

Number of letters in database: 19,553,006

Number of sequences in database: 119,193

Lambda	K	H
0.309	0.123	0.353

**Gapped**

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 442,228

Number of Sequences: 119193

Number of extensions: 1918

Number of successful extensions: 6

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 5

Number of HSP's gapped (non-prelim): 1

length of query: 15

length of database: 19,553,006

effective HSP length: 0

effective length of query: 24

effective length of database: 19,553,006

effective search space: 469272144  
effective search space used: 469272144  
T: 11  
A: 40  
X1: 16 ( 7.1 bits)  
X2: 38 (14.6 bits)  
X3: 64 (24.7 bits)  
S1: 42 (21.8 bits)  
S2: 55 (25.8 bits)